

#2



OIPF

RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/997,701

TIME: 16:39:44

Input Set : N:\Crf3\RULE60\09997701.raw

Output Set: N:\CRF3\01282002\I997701.raw

1 <110> APPLICANT: Yue, Henry
 2 Corley, Neil C.
 3 Guegler, Karl J.
 4 Gorgone, Gina A.
 5 Baughn, Mariah R.
 6 <120> TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
 7 <130> FILE REFERENCE: PF-0631 US
 8 <140> CURRENT APPLICATION NUMBER: 09/997,701
 9 <141> CURRENT FILING DATE: 2001-11-30
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/470,946
 W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
 12 <160> NUMBER OF SEQ ID NOS: 6
 13 <170> SOFTWARE: PERL Program
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 16 <211> LENGTH: 195
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Homo sapiens
 W--> 19 <220> FEATURE: -
 20 <223> OTHER INFORMATION: 2297891
 21 <400> SEQUENCE: 1
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 23 1 5 10 15
 24 Leu Met His Ala Arg Gly Gln Arg Asp Phe Asp Leu Ala Asp Ala
 25 20 25 30
 26 Leu Asp Asp Pro Glu Pro Thr Lys Lys Pro Asn Ser Asp Ile Tyr
 27 35 40 45
 28 Pro Lys Pro Lys Pro Pro Tyr Tyr Pro Gln Pro Glu Asn Pro Asp
 29 50 55 60
 30 Ser Gly Gly Asn Ile Tyr Pro Arg Pro Lys Pro Arg Pro Gln Pro
 31 65 70 75
 32 Gln Pro Gly Asn Ser Gly Asn Ser Gly Gly Tyr Phe Asn Asp Val
 33 80 85 90
 34 Asp Arg Asp Asp Gly Arg Tyr Pro Pro Arg Pro Arg Pro Arg Pro
 35 95 100 105
 36 Pro Ala Gly Gly Gly Gly Gly Gly Tyr Ser Ser Tyr Gly Asn Ser
 37 110 115 120
 38 Asp Asn Thr His Gly Arg Gly Gly Tyr Arg Pro Asn Ser Arg Tyr
 39 125 130 135
 40 Gly Asn Thr Tyr Gly Gly Asp His His Ser Thr Tyr Gly Asn Pro
 41 140 145 150
 42 Glu Gly Asn Met Val Ala Lys Ile Val Ser Pro Ile Val Ser Val
 43 155 160 165
 44 Val Val Val Thr Leu Leu Gly Ala Ala Ala Ser Tyr Phe Lys Leu

ENTERED

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46      Asn Asn Arg Arg Asn Cys Phe Arg Thr His Glu Pro Glu Asn Val
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51 <212> TYPE: PRT
52 <213> ORGANISM: Homo sapiens
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54 <223> OTHER INFORMATION: 2705267
55 <400> SEQUENCE: 2
56      Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly
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58      Leu Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu
59          20          25          30
60      Leu Asp Gly Phe Arg Ser Asp Tyr Ile Ser Asp Glu Ala Leu Glu
61          35          40          45
62      Ser Leu Pro Gly Phe Lys Glu Ile Val Ser Arg Gly Val Lys Val
63          50          55          60
64      Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu Ser Tyr Pro Asn Tyr
65          65          70          75
66      Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val His Gln Met Ile
67          80          85          90
68      Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser Phe Asp Ile
69          95          100          105
70      Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn Gly Ser
71          110          115          120
72      Glu Pro Leu Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val Tyr
73          125          130          135
74      Met Tyr Tyr Trp Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg
75          140          145          150
76      Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn
77          155          160          165
78      Phe Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly
79          170          175          180
80      Arg Ala Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu
81          185          190          195
82      Gly His His Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu
83          200          205          210
84      Lys Ala Val Asp Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln
85          215          220          225
86      Glu Arg Gly Leu Gln Asp Arg Leu Asn Val Ile Ile Phe Ser Asp
87          230          235          240
88      His Gly Met Thr Asp Ile Phe Trp Met Asp Lys Val Ile Glu Leu
89          245          250          255
90      Asn Lys Tyr Ile Ser Leu Asn Asp Leu Gln Gln Val Lys Asp Arg
91          260          265          270
92      Gly Pro Val Val Ser Leu Trp Pro Ala Pro Gly Lys His Ser Glu
93          275          280          285
94      Ile Tyr Asn Lys Leu Ser Thr Val Glu His Met Thr Val Tyr Glu

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Input Set : N:\Crif3\RULE60\09997701.raw

Output Set: N:\CRF3\01282002\I997701.raw

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95          290          295          300
96      Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr Lys Lys Gly Lys Phe
97          305          310          315
98      Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly Trp Phe Ile Thr
99          320          325          330
100      Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser Thr Gly Arg
101          335          340          345
102      Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn Glu Leu
103          350          355          360
104      Met Asp Met Arg Gly Ile Phe Leu Thr Leu Gly Pro Gly Arg Arg
105          365          370          375
106      Gly Asn Asp Gln Met Leu Ser Asp Pro Ile Pro Lys Glu Val Ser
107          380          385          390
108      Leu Arg Gly Pro Thr Gly Ala Arg Arg Gly Cys Arg Asp Phe Leu
109          395          400          405
110      Thr Asp Pro Leu Tyr Glu Pro Ser Arg Ala Asn Pro Ala Gly Leu
111          410          415          420
112      His Glu Thr Ser Phe Ala Gly Phe Leu Ser Asn Ala Ser Trp Val
113          425          430          435
114      Trp Gln Met
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117 <211> LENGTH: 935
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
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121 <223> OTHER INFORMATION: 2297891
122 <400> SEQUENCE: 3
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124      actggtccca caggttttca gctgtggagt ttgggatctg agcttggagc ccatttgttt 120
125      ctggcagttc cgctcatatt ttccacttga agacatcgcc tcccttcctt ccaagctggg 180
126      agaccagaag tcaacaacag gaggggtggag aggcggggtc tcacaatccg cttggctggg 240
127      gagtccactg aggttcttgc atcctgaagc aaaccatgga gagctggtgg ggacttccct 300
128      gtcttgcggt cctgtgtttt ctaatgcacg ccgaggttca aagagacttt gatttggcag 360
129      atgcccttga tgaccctgaa cccaccaaga agccaaaactc agatatctac ccaaagccaa 420
130      aaccacctta ctaccacag cccgagaatc ccgacagcgg tggaaatatc tacccaaggc 480
131      caaagccacg cctcaaccc cagcctggca attccggcaa cagtggaggt tacttcaatg 540
132      atgtggaccg tgatgacgga cgctaccgc ccaggcccag gccacggccg cctgcaggag 600
133      gtggcggcgg tggctactcc agttatggca actccgacaa cagcacgga agagggggct 660
134      atagacccaa ctctcggttat ggaaatactt atggtggaga tcaccattca acgtatggca 720
135      atccagaagg caatatggta gcaaaaatcg tgtctcccat cgtatccgtg gtgggtggta 780
136      cactgctggg agcagcagcc agttatttca aactaaacaa taggagaaat tgtttcagga 840
137      cccatgaacc agaaaatgtc tgaagatgtt aagatcccct gattactttg ggaaaaacaa 900
138      ctaaaacaag aaccgtgttt atcaaaaaaa aaaaa 935
140 <210> SEQ ID NO: 4
141 <211> LENGTH: 1438
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
W--> 144 <220> FEATURE: -
145 <223> OTHER INFORMATION: 2705267

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149 ccctgggcct ggcccagcca gcctctgccc gccggaagct gctggtgttt ctgctggatg 180
150 gttttcgctc agactacatc agtgatgagg cgctggagtc attgcctggt ttcaaagaga 240
151 ttgtgagcag gggagtaaaa gtggattact tgactccaga cttccctagt ctctcgatc 300
152 ccaattatta taccctaatt actggccgcc attgtgaagt ccatcagatg atcgggaact 360
153 acatgtggga cccaccacc aacaagtcct ttgacattgg cgtcaacaaa gacagcctaa 420
154 tgctctctg gtggaatgga tcagaacctc tgtgggtcac tctgaccaag gccaaaagga 480
155 aggtctacat gtactactgg ccaggctgtg aggttgagat tctgggtgtc agaccacct 540
156 actgcctaga atataaaaat gtcccaacgg atatcaattt tgccaatgca gtcagcgatg 600
157 ctcttgactc cttcaagagt ggccgggccc acctggcagc catataccat gagcgcatg 660
158 acgtggaagg ccaccactac gggcctgcat ctccgcagag gaaagatgcc ctcaaggctg 720
159 tagacactgt cctgaagtac atgaccaagt ggatccagga gcggggcctg caggaccgcc 780
160 tgaacgtcat tattttctcg gatcacggaa tgaccgacat tttctggatg gacaaagtga 840
161 ttgagctgaa taagtacatc agcctgaatg acctgcagca agtgaaggac cgcgggcctg 900
162 ttgtgagcct ttggccggcc cctgggaaac actctgagat atatacaaaa ctgagcacag 960
163 tggaacacat gactgtctac gagaaagaag ccatcccaag caggttctat tacaagaaag 1020
164 gaaagtttgt ctctcctttg actttagtgg ctgatgaagg ctgggtcata actgagaatc 1080
165 gagagatgct tccgttttgg atgaacagca ccggcaggcg ggaaggttgg cagcgtggat 1140
166 ggacaggcta cgacaacgag ctcatggaca tgcggggcat ctctcctgact ctcgacactg 1200
167 gtaggcgagg aaatgaccag atgctctcag accccattcc caaggaagtg tctctaaggg 1260
168 gccctacggg tgccaggaga ggctgcaggg atttccctcac agaccctctt tatgagccaa 1320
169 gcagagcaaa cccagccggt ctccatgaaa catcttttgc tggcttcctt tcaaatgctt 1380
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173 <211> LENGTH: 180

174 <212> TYPE: PRT

175 <213> ORGANISM: Homo sapiens

W--> 176 <220> FEATURE: -

177 <223> OTHER INFORMATION: g2499136

178 <400> SEQUENCE: 5

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182 20 25 30
183 Leu Asp Asp Pro Gly Pro Thr Lys Lys Pro Asn Ser Asp Ile Tyr
184 35 40 45
185 Pro Lys Pro Lys Pro Pro Tyr Tyr Pro Gln Pro Glu Asn Pro Asp
186 50 55 60
187 Ser Gly Gly Asn Ile Tyr Pro Arg Pro Lys Pro Arg Pro Gln Pro
188 65 70 75
189 Gln Pro Gly Asn Ser Gly Asn Ser Gly Gly Tyr Phe Asn Asp Val
190 80 85 90
191 Asp Arg Asp Asp Gly Arg Tyr Pro Pro Arg Pro Arg Pro Arg Pro
192 95 100 105
193 Pro Ala Gly Gly Gly Gly Gly Tyr Ser Ser Tyr Gly Asn Ser
194 110 115 120
195 Asp Asn Thr His Gly Gly Asp His His Ser Thr Tyr Gly Asn Pro

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Output Set: N:\CRF3\01282002\I997701.raw

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196          125          130          135
197      Glu Gly Asn Met Val Ala Lys Ile Val Ser Pro Ile Val Ser Val
198          140          145          150
199      Val Val Val Thr Leu Leu Gly Ala Ala Ala Ser Tyr Phe Lys Leu
200          155          160          165
201      Asn Asn Arg Arg Asn Cys Phe Arg Thr His Glu Pro Glu Asn Val
202          170          175          180
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205 <211> LENGTH: 873
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
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209 <223> OTHER INFORMATION: gl89650
210 <400> SEQUENCE: 6
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213      Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu Val Leu
214          20          25          30
215      Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly Leu
216          35          40          45
217      Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
218          50          55          60
219      Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val
220          65          70          75
221      Glu Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu
222          80          85          90
223      Pro Glu His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys
224          95          100          105
225      Arg Leu Thr Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp
226          110          115          120
227      Lys Gly Asp Cys Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu
228          125          130          135
229      Lys Ser Trp Val Glu Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln
230          140          145          150
231      Cys Pro Ala Gly Phe Glu Thr Pro Pro Thr Leu Leu Phe Ser Leu
232          155          160          165
233      Asp Gly Phe Arg Ala Glu Tyr Leu His Thr Trp Gly Gly Leu Leu
234          170          175          180
235      Pro Val Ile Ser Lys Leu Lys Lys Cys Gly Thr Tyr Thr Lys Asn
236          185          190          195
237      Met Arg Pro Val Tyr Pro Thr Lys Thr Phe Pro Asn His Tyr Ser
238          200          205          210
239      Ile Val Thr Gly Leu Tyr Pro Glu Ser His Gly Ile Ile Asp Asn
240          215          220          225
241      Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe Ser Leu Lys Ser
242          230          235          240
243      Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu Pro Ile Trp
244          245          250          255
245      Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe Phe Trp

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VERIFICATION SUMMARY

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TIME: 16:39:45

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